

allow gaps of up to 5% of the total number of residues in amino acids 2 to 242 of SEQ ID NO:2.

28. The isolated polynucleotide of claim 27, comprising a nucleotide sequence encoding amino acids 2 to 242 of SEQ ID NO:2.

29. The isolated polynucleotide of claim 28, comprising nucleotides 3875 to 4597 of SEQ ID NO:1.

30. The isolated polynucleotide of claim 27, wherein said amino acid sequence is at least 95% identical to amino acids 1 to 242 of SEQ ID NO:2;

wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of amino acids 1 to 242 of SEQ ID NO:2 and that allow gaps of up to 5% of the total number of residues in amino acids 1 to 242 of SEQ ID NO:2.

31. The isolated polynucleotide of claim 30, comprising a nucleotide sequence encoding amino acids 1 to 242 of SEQ ID NO:2.

32. The isolated polynucleotide of claim 31, comprising nucleotides 3872 to 4597 of SEQ ID NO:1.

33. The isolated polynucleotide of claim 27, further comprising a heterologous polynucleotide.

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CONT'D.

34. The isolated polynucleotide of claim 33, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

35. A method of producing a vector that comprises inserting the isolated polynucleotide of claim 27 into a vector.

36. A vector comprising the isolated polynucleotide of claim 27.

37. The vector of claim 36, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

38. A host cell comprising the isolated polynucleotide of claim 27.

39. The host cell of claim 38, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

40. A method of producing a polypeptide that comprises culturing the host cell of claim 39 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

41. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide, the sequence of which is at least 95% identical to a reference amino acid sequence selected from the group consisting of:

(a) amino acids 15 to 36 of SEQ ID NO:2;

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- C1
CONT'D.
- (b) amino acids 42 to 62 of SEQ ID NO:2;
 - (c) amino acids 35 to 95 of SEQ ID NO:2;
 - (d) amino acids 219 to 240 of SEQ ID NO:2; and
 - (e) amino acids 96 to 218 of SEQ ID NO:2;

wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of the reference amino acid sequence and that allow gaps in homology of up to 5% of the total number of residues in the reference amino acid sequence.

42. The isolated polynucleotide of claim 41, which comprises a polynucleotide encoding an amino acid sequence at least 95% identical to the amino acid sequence of (a).

43. The isolated polynucleotide of claim 42, which comprises a nucleotide sequence encoding the amino acid sequence of (a).

44. The isolated polynucleotide of claim 43, which comprises nucleotides 3914 to 3979 of SEQ ID NO:1.

45. The isolated polynucleotide of claim 41, which comprises a nucleotide sequence encoding an amino acid sequence at least 95% identical to the amino acid sequence of (b).

46. The isolated polynucleotide of claim 45, which comprises a nucleotide sequence encoding the amino acid sequence of (b).

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CONT'D

47. The isolated polynucleotide of claim 46, which comprises nucleotides 3995 to 4057 of SEQ ID NO:1.

48. The isolated polynucleotide of claim 41, which comprises a nucleotide sequence encoding g an amino acid sequence at least 95% identical to the amino acid sequence of (c).

49. The isolated polynucleotide of claim 48, which comprises a nucleotide sequence encoding the amino acid sequence of (c).

50. The isolated polynucleotide of claim 49, which comprises nucleotides 3974 to 4156 of SEQ ID NO:1.

51. The isolated polynucleotide of claim 41, which comprises a nucleotide sequence encoding an amino acid sequence at least 95% identical to the amino acid sequence of (d).

52. The isolated polynucleotide of claim 51, which comprises a nucleotide sequence encoding the amino acid sequence of (d).

53. The isolated polynucleotide of claim 52, which comprises nucleotides 4526 to 4591 of SEQ ID NO:1.

54. The isolated polynucleotide of claim 41, which comprises a nucleotide sequence encoding g an amino acid sequence at least 95% identical to the amino acid sequence of (e).

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CONT'D.

55. The isolated polynucleotide of claim 54, which comprises a nucleotide sequence encoding the amino acid sequence of (e).

56. The isolated polynucleotide of claim 55, which comprises nucleotides 4157 to 4526 of SEQ ID NO:1.

57. The isolated polynucleotide of claim 41, further comprising a heterologous polynucleotide.

58. The isolated polynucleotide of claim 57, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

59. A method of producing a vector that comprises inserting the isolated polynucleotide of claim 41 into a vector.

60. A vector comprising the isolated polynucleotide of claim 41.

61. The vector of claim 60, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

62. A host cell comprising the isolated polynucleotide of claim 41.

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CONT'D.

63. The host cell of claim 62, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

64. A method of producing a polypeptide that comprises culturing the host cell of claim 63 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

65. An isolated polynucleotide comprising a first polynucleotide which hybridizes to a second polynucleotide consisting of the nucleotide sequence of the coding region of SEQ ID NO:1, or the full-length complement thereof, under conditions comprising:

(a) incubating overnight at 42°C in a solution consisting of 50% formamide, 5x SSC, 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA; and

(b) washing at 65°C in a solution consisting of 0.1x SSC;
wherein said first polynucleotide is at least 70 nucleotides in length.

66. The isolated polynucleotide of claim 65, further comprising a heterologous polynucleotide.

67. The isolated polynucleotide of claim 66, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

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CONT'D.

68. A method of producing a vector that comprises inserting the isolated polynucleotide of claim 65 into a vector.

69. A vector comprising the isolated polynucleotide of claim 65.

70. The vector of claim 69, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

71. A host cell comprising the isolated polynucleotide of claim 65.

72. The host cell of claim 71, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

73. A method of producing a polypeptide that comprises culturing the host cell of claim 72 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

74. An isolated polynucleotide comprising 60 contiguous nucleotides of the coding region of SEQ ID NO:1.

75. The isolated polynucleotide of claim 74, wherein said sequence comprises 70 contiguous nucleotides of SEQ ID NO:1.

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CONT'D.

76. The isolated polynucleotide of claim 75, wherein said sequence comprises 150 contiguous nucleotides of SEQ ID NO:1.

77. The isolated polynucleotide of claim 74, further comprising a heterologous polynucleotide.

78. The isolated polynucleotide of claim 77, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

79. A method of producing a vector that comprises inserting the isolated polynucleotide of claim 74 into a vector.

80. A vector comprising the isolated polynucleotide of claim 74.

81. The vector of claim 80, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

82. A host cell comprising the isolated polynucleotide of claim 74.

83. The host cell of claim 82, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

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CONTD.

84. A method of producing a polypeptide that comprises culturing the host cell of claim 83 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

85. An isolated polynucleotide encoding a polypeptide comprising at least 30 contiguous amino acids of SEQ ID NO:2, or an isolated polynucleotide having a nucleotide sequence complementary thereto.

86. The isolated polynucleotide of claim 85 wherein said polypeptide comprises at least 50 contiguous amino acids of SEQ ID NO:2, or an isolated polynucleotide having a nucleotide sequence complementary thereto.

87. The isolated polynucleotide of claim 85, further comprising a heterologous polynucleotide.

88. The isolated polynucleotide of claim 87, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

89. A method of producing a vector that comprises inserting the isolated polynucleotide of claim 85 into a vector.

90. A vector comprising the isolated polynucleotide of claim 85.

91. The vector of claim 90, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

92. A host cell comprising the isolated polynucleotide of claim 85.

93. The host cell of claim 92, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

94. A method of producing a polypeptide that comprises culturing the host cell of claim 93 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

95. An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to amino acids 1 to 260 of SEQ ID NO:42;

wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of amino acids 1 to 260 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids 1 to 260 of SEQ ID NO:42.

2 96. The isolated polynucleotide of claim 95, comprising a nucleotide sequence encoding amino acids 1 to 260 of SEQ ID NO:42.

3 97. The isolated polynucleotide of claim 96, comprising nucleotides 95 to 874 of SEQ ID NO:41.

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CONT'D.
P2

98. The isolated polynucleotide of claim 95, wherein said amino acid sequence is at least 95% identical to amino acids 1 to 488 of SEQ ID NO:42;

wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of amino acids 1 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids 1 to 488 of SEQ ID NO:42.

5 4
~~99.~~ The isolated polynucleotide of claim ~~98~~, comprising a nucleotide sequence encoding amino acids 1 to 488 of SEQ ID NO:42.

6 5
~~100.~~ The isolated polynucleotide of claim ~~99~~, comprising nucleotides 95 to 1558 of SEQ ID NO:41.

101. The isolated polynucleotide of claim 98, wherein said amino acid sequence is at least 95% identical to amino acids -17 to 488 of SEQ ID NO:42;

P2
D3

wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of amino acids -17 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids -17 to 488 of SEQ ID NO:42.

8 7
~~102.~~ The isolated polynucleotide of claim ~~101~~, comprising a nucleotide sequence encoding amino acids -17 to 488 of SEQ ID NO:42.

⁹
~~103.~~ The isolated polynucleotide of claim 102, comprising nucleotides 44 to 1558 of SEQ ID NO:41.

¹⁰
~~104.~~ The isolated polynucleotide of claim 101, wherein said amino acid sequence is at least 95% identical to amino acids -18 to 488 of SEQ ID NO:42;

wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of amino acids -18 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids -18 to 488 of SEQ ID NO:42.

¹¹
~~105.~~ The isolated polynucleotide of claim ~~104~~, comprising a nucleotide sequence encoding amino acids -18 to 488 of SEQ ID NO:42.

¹²
~~106.~~ The isolated polynucleotide of claim ~~105~~, comprising nucleotides 41 to 1558 of SEQ ID NO:41.

¹³
~~107.~~ The isolated polynucleotide of claim ~~95~~, further comprising a heterologous polynucleotide.

¹⁴
~~108.~~ The isolated polynucleotide of claim ~~107~~, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

¹⁵
~~109.~~ A method of producing a vector that comprises inserting the isolated polynucleotide of claim ~~95~~ into a vector.

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CONT'D.
- ~~16~~
~~110.~~ A vector comprising the isolated polynucleotide of claim ~~95~~.
- ~~17~~ ~~16~~
~~111.~~ The vector of claim ~~110~~, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.
- ~~18~~
~~112.~~ A host cell comprising the isolated polynucleotide of claim ~~95~~.
- ~~19~~ ~~18~~
~~113.~~ The host cell of claim ~~112~~, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.
- ~~20~~
~~114.~~ A method of producing a polypeptide that comprises culturing the host cell of claim ~~113~~ under conditions such that said polypeptide is expressed, and recovering said polypeptide.

115. An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642,

Ans
DS

wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of residues of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

²²
~~116.~~ The isolated polynucleotide of claim ~~115~~²¹, comprising a nucleotide sequence encoding the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

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CONT'D.

117. The isolated polynucleotide of claim 115, wherein said amino acid sequence is at least 95% identical to the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642;

And
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wherein % identity is determined using the Bestfit program with parameters that calculate % identity over the full length of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of residues of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

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Sub 37
~~118.~~ The isolated polynucleotide of claim ~~117~~, comprising the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

²⁵
~~119.~~ The isolated polynucleotide of claim ~~118~~²¹, further comprising a heterologous polynucleotide.

²⁶
~~120.~~ The isolated polynucleotide of claim ~~119~~²⁵, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

²⁷
~~121.~~ A method of producing a vector that comprises inserting the isolated polynucleotide of claim ~~118~~²¹ into a vector.

²⁸
~~122.~~ A vector comprising the isolated polynucleotide of claim ~~118~~²¹.

²⁹
~~123.~~ The vector of claim ~~122~~²⁸, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

³⁰
~~124.~~ A host cell comprising the isolated polynucleotide of claim ~~118~~²¹.

³¹
~~125.~~ The host cell of claim ~~124~~³⁰, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

³²
~~126.~~ A method of producing a polypeptide that comprises culturing the host cell of claim ~~125~~³¹ under conditions such that said polypeptide is expressed, and recovering said polypeptide.

127. An isolated polynucleotide comprising a first polynucleotide which hybridizes to a second polynucleotide consisting of the nucleotide sequence of the coding region of SEQ ID NO:41, or the full-length complement thereof, under conditions comprising:

(a) incubating overnight at 42°C in a solution consisting of 50% formamide, 5x SSC, 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA; and

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(b) washing at 65°C in a solution consisting of 0.1x SSC;
wherein said first polynucleotide is at least 70 nucleotides in length.

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CONT'D.

~~34~~ 128. The isolated polynucleotide of claim ~~127~~³³, further comprising a heterologous polynucleotide.

~~35~~ 129. The isolated polynucleotide of claim ~~128~~³⁴, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

~~36~~ 130. A method of producing a vector that comprises inserting the isolated polynucleotide of claim ~~127~~³³ into a vector.

~~37~~ 131. A vector comprising the isolated polynucleotide of claim ~~127~~³³.

~~38~~ 132. The vector of claim ~~131~~³⁷, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

~~39~~ 133. A host cell comprising the isolated polynucleotide of claim ~~127~~³³.

~~40~~ 134. The host cell of claim ~~133~~³⁹, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

⁴¹
~~135.~~ A method of producing a polypeptide that comprises culturing the host cell of claim ~~134~~⁴⁰ under conditions such that said polypeptide is expressed, and recovering said polypeptide.

⁴²
~~136.~~ An isolated polynucleotide comprising 60 contiguous nucleotides of the coding region of SEQ ID NO:41.

⁴³
~~137.~~ The isolated polynucleotide of claim ~~136~~⁴², wherein said sequence comprises 70 contiguous nucleotides of SEQ ID NO:41.

⁴⁴
~~138.~~ The isolated polynucleotide of claim ~~137~~⁴³, wherein said sequence comprises 100 contiguous nucleotides of SEQ ID NO:41.

⁴⁵
~~139.~~ The isolated polynucleotide of claim ~~138~~⁴⁴, wherein said sequence comprises 200 contiguous nucleotides of SEQ ID NO:41.

⁴⁶
~~140.~~ The isolated polynucleotide of claim ~~139~~⁴⁵, further comprising a heterologous polynucleotide.

⁴⁷
~~141.~~ The isolated polynucleotide of claim ~~140~~⁴⁶, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

⁴⁸
~~142.~~ A method of producing a vector that comprises inserting the isolated polynucleotide of claim ~~141~~⁴⁷ into a vector.

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CONT'D.

⁴⁹
~~143.~~ A vector comprising the isolated polynucleotide of claim ⁴²~~136~~.

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CONT'D.
⁴⁹
~~50~~ ~~144.~~ The vector of claim ~~143~~, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

⁴²
~~51~~ ~~145.~~ A host cell comprising the isolated polynucleotide of claim ~~136~~.

⁵¹
~~52~~ ~~146.~~ The host cell of claim ~~145~~, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

⁵²
~~53~~ ~~147.~~ A method of producing a polypeptide that comprises culturing the host cell of claim ~~146~~ under conditions such that said polypeptide is expressed, and recovering said polypeptide.

148. An isolated polynucleotide encoding a polypeptide comprising at least 30 contiguous amino acids of SEQ ID NO:2, or an isolated polynucleotide having a nucleotide sequence complementary thereto.

149. The isolated polynucleotide of claim 148 wherein said polypeptide comprises at least 50 contiguous amino acids of SEQ ID NO:2, or an isolated polynucleotide having a nucleotide sequence complementary thereto.

150. The isolated polynucleotide of claim 148, further comprising a heterologous polynucleotide.

151. The isolated polynucleotide of claim 150, wherein said heterologous polynucleotide encodes a heterologous polypeptide.

152. A method of producing a vector that comprises inserting the isolated polynucleotide of claim 148 into a vector.

153. A vector comprising the isolated polynucleotide of claim 148.

154. The vector of claim 153, wherein said polynucleotide is operably associated with a heterologous regulatory sequence.

155. A host cell comprising the isolated polynucleotide of claim 148.

156. The host cell of claim 155, wherein said isolated polynucleotide is operably associated with a heterologous regulatory sequence.

157. A method of producing a polypeptide that comprises culturing the host cell of claim 156 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

Remarks

After cancellation of claims 1-9 and 11-26 and entry of the foregoing amendments, claims 10 and 27-157 will be pending in the application, with claims 10, 27, 41, 65, 74, 85, 95, 115, 127, 136 and 148 being the independent claims.